

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,125
Source: IFWP
Date Processed by STIC: 5/24/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/24/2006

PATENT APPLICATION: US/10/579,125

TIME: 12:19:21

Input Set : A:\42-000500us sequence listing.txt

Output Set: N:\CRF4\05242006\J579125.raw

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3 <110> APPLICANT: James, David
4   Cooney, Gregory J
5   Molero-Navajas, Juan C
7 <120> TITLE OF INVENTION: Methods of validating target for modulating insulin action,
8   screening for modulators of insulin action and therapeutic uses
9   thereof
11 <130> FILE REFERENCE: 42-000500US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/579,125
C--> 13 <141> CURRENT FILING DATE: 2006-05-12
13 <150> PRIOR APPLICATION NUMBER: AU 2003906286
14 <151> PRIOR FILING DATE: 2003-11-14
16 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/001572
17 <151> PRIOR FILING DATE: 2004-11-15
19 <150> PRIOR APPLICATION NUMBER: AU 2003906285
20 <151> PRIOR FILING DATE: 2003-11-14
22 <160> NUMBER OF SEQ ID NOS: 268
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 153
28 <212> TYPE: PRT
29 <213> ORGANISM: Mus musculus
31 <400> SEQUENCE: 1
33 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Gly Ser
34 1          5          10          15
37 Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe
38          20          25          30
41 Gln Pro His His His His His His Leu Ser Pro His Pro Pro Cys Thr
42          35          40          45
45 Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val
46          50          55          60
49 Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro
50 65          70          75          80
53 Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val
54          85          90          95
57 Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr
58          100         105         110
61 Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile
62          115         120         125
65 Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln
66          130         135         140
69 Pro Arg Arg Asn Leu Thr Lys Leu Ser
70 145         150
73 <210> SEQ ID NO: 2

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74 <211> LENGTH: 896
75 <212> TYPE: PRT
76 <213> ORGANISM: Mus musculus
78 <400> SEQUENCE: 2
80 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Gly Ser
81 1 5 10 15
84 Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe
85 20 25 30
88 Gln Pro His His His His His His Leu Ser Pro His Pro Pro Cys Thr
89 35 40 45
92 Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val
93 50 55 60
96 Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro
97 65 70 75 80
100 Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val
101 85 90 95
104 Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr
105 100 105 110
108 Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile
109 115 120 125
112 Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln
113 130 135 140
116 Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His Met Leu
117 145 150 155 160
120 Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly Asp Thr
121 165 170 175
124 Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys Ala Phe
125 180 185 190
128 Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala Leu His
129 195 200 205
132 Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu Lys Ser
133 210 215 220
136 Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu Phe Asp
137 225 230 235 240
140 Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg Asn Trp
141 245 250 255
144 Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu Thr Tyr
145 260 265 270
148 Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro Gly Ser
149 275 280 285
152 Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala Ile Gly
153 290 295 300
156 Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His Asn Lys
157 305 310 315 320
160 Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe Tyr Leu
161 325 330 335
164 Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu Cys Glu
165 340 345 350
168 Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Ile Cys Ala Glu Asn

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169          355          360          365
172 Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser
173          370          375          380
176 Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys
177 385          390          395          400
180 Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp Pro Phe Asp
181          405          410          415
184 Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu Gly Ala Pro
185          420          425          430
188 Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp Asp Ser Leu
189          435          440          445
192 Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg Pro Ser Ser
193          450          455          460
196 Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val Pro Pro Arg
197 465          470          475          480
200 Leu Asp Leu Leu Gln Arg Ala Pro Val Pro Ala Ser Thr Ser Val
201          485          490          495
204 Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His Lys Asp Lys
205          500          505          510
208 Pro Leu Pro Ile Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro
209          515          520          525
212 Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Thr Arg Pro Gln Arg Arg
213          530          535          540
216 Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp Lys Leu Pro
217 545          550          555          560
220 Pro Val Pro Ser Ser Arg Pro Gly Asp Ser Trp Leu Ser Arg Thr Ile
221          565          570          575
224 Pro Lys Val Pro Val Ala Thr Pro Asn Pro Gly Asp Pro Trp Asn Gly
225          580          585          590
228 Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu Pro Ser Gln
229          595          600          605
232 Met Glu Pro Arg Ala Asp Val Pro Arg Leu Gly Ser Thr Phe Ser Leu
233          610          615          620
236 Asp Thr Ser Met Thr Met Asn Ser Ser Pro Val Ala Gly Pro Glu Ser
237 625          630          635          640
240 Glu His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala Ile Tyr Ser
241          645          650          655
244 Leu Ala Ala Arg Pro Leu Pro Met Pro Lys Leu Pro Pro Gly Glu Gln
245          660          665          670
248 Gly Glu Ser Glu Glu Asp Thr Glu Tyr Met Thr Pro Thr Ser Arg Pro
249          675          680          685
252 Val Gly Val Gln Lys Pro Glu Pro Lys Arg Pro Leu Glu Ala Thr Gln
253          690          695          700
256 Ser Ser Arg Ala Cys Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr
257 705          710          715          720
260 Glu Ala Met Tyr Thr Ile Gln Ser Gln Ala Leu Ser Val Ala Glu Asn
261          725          730          735
264 Ser Ala Ser Gly Glu Gly Asn Leu Ala Thr Ala His Thr Ser Thr Gly
265          740          745          750

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```

268 Pro Glu Glu Ser Glu Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro
269      755      760      765
272 Pro Val Pro Ala Val Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn
273      770      775      780
276 Ala Ser Ser Ser Phe Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Asn
277 785      790      795      800
280 Phe Asn Glu Gly Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro
281      805      810      815
284 Arg Arg Ile Asn Ser Glu Arg Lys Ala Ser Ser Tyr Gln Gln Gly Gly
285      820      825      830
288 Gly Ala Thr Ala Asn Pro Val Ala Thr Ala Pro Ser Pro Gln Leu Ser
289      835      840      845
292 Ser Glu Ile Glu Arg Leu Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile
293      850      855      860
296 Gln Lys Ala Leu Val Ile Ala His Asn Asn Ile Glu Met Ala Lys Asn
297 865      870      875      880
300 Ile Leu Arg Glu Phe Val Ser Ile Ser Ser Pro Ala His Val Ala Thr
301      885      890      895
304 <210> SEQ ID NO: 3
305 <211> LENGTH: 906
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 3
311 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
312 1      5      10      15
315 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
316      20      25      30
319 Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro
320      35      40      45
323 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
324      50      55      60
327 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
328 65      70      75      80
331 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
332      85      90      95
335 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
336      100      105      110
339 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
340      115      120      125
343 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
344      130      135      140
347 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
348 145      150      155      160
351 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
352      165      170      175
355 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
356      180      185      190
359 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
360      195      200      205

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```

363 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
364      210                      215                      220
367 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
368 225                      230                      235                      240
371 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
372                      245                      250                      255
375 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
376                      260                      265                      270
379 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
380                      275                      280                      285
383 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
384      290                      295                      300
387 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
388 305                      310                      315                      320
391 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
392                      325                      330                      335
395 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
396                      340                      345                      350
399 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
400                      355                      360                      365
403 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
404      370                      375                      380
407 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
408 385                      390                      395                      400
411 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
412                      405                      410                      415
415 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
416                      420                      425                      430
419 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
420                      435                      440                      445
423 Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp
424      450                      455                      460
427 Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
428 465                      470                      475                      480
431 Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
432                      485                      490                      495
435 Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
436                      500                      505                      510
439 Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
440                      515                      520                      525
443 Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
444      530                      535                      540
447 Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro
448 545                      550                      555                      560
451 Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp
452                      565                      570                      575
455 Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro
456                      580                      585                      590
459 Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/579,125

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Input Set : A:\42-000500us sequence listing.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31
Seq#:32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79
Seq#:80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120
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Seq#:247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,264,265
Seq#:266,267,268

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/579,125**

DATE: 05/24/2006

TIME: 12:19:22

Input Set : **A:\42-000500us sequence listing.txt**

Output Set: **N:\CRF4\05242006\J579125.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date